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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=6; hr=8; min=54; sec=0; ms=423; ]

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Reviewer Comments:

<210> 5

<211> 87

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<223> Xaa = Tyr, Val, Ile, Leu, Met, Phe, Trp

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<223> Xaa = Asn, His, Gln, Cys, Ser, Thr

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<222> (5)...(5)

<223> Xaa = any amino acid residue

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20 25 30  
Xaa Xaa Leu Leu Arg Xaa His Xaa Xaa Leu Xaa Xaa Ala Xaa Xaa Arg  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Leu Val Xaa Xaa Xaa Xaa Xaa Leu  
50 55 60  
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Xaa Ala Xaa Xaa Xaa Lys Val  
85

The "<213> Artificial Sequence" needs explanation in a <220>-<223>  
section; please give the source of the genetic material. Same error in  
Sequences 6-7.

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Application No: 10573372 Version No: 3.0

Input Set:

Output Set:

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Finished: 2009-05-05 15:29:15.521  
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 37 ms  
Total Warnings: 3  
Total Errors: 3  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

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<110> Dale, James Langham  
Echeverria, Santy Peraza

<130> DAVI172.006APC

<141> 2009-05-05

<151> 2004-09-23

<151> 2003-09-25

<170> FastSEQ for Windows Version 4.0

<211> 4380

<212> DNA

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$\langle 222 \rangle$  (1) . . (4323)

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Gln Thr Leu Leu Asp Lys Ala Ser Asn Cys Ala Ile Gln Gln Leu Ala  
20 25 30

cgg cgc cgc ggc ctt cac gat gac ctg agg cgg ctg cgg acg tct ctg 144  
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35 40 45

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Leu Arg Ile His Ala Ile Leu Asp Lys Ala Glu Thr Arg Trp Asn His  
50 55 60

aaa aac acg agc ttg gtg gag ctg gtg agg cag ctc aag gat gct gcc 240  
Lys Asn Thr Ser Leu Val Glu Leu Val Arg Gln Leu Lys Asp Ala Ala  
65 70 75 80

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100 105 110	
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115 120 125	
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Gly Thr Arg Leu Arg Glu Ile Gln Gly Lys Leu Cys Asn Ile Ala Ala	
130 135 140	
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Asp Met Met Asp Val Met Gln Leu Leu Ala Pro Asp Asp Gly Gly Arg	
145 150 155 160	
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Glu Thr Val Val Phe Gly Arg Asp Gln Glu Arg Glu Lys Val Val Glu	
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Tyr Asn Asp Asn Arg Val Gly Asn Tyr Phe His Leu Lys Val Trp Val	
225 230 235 240	
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Cys Val Ser Asp Asn Phe Asn Val Lys Arg Leu Thr Lys Glu Ile Ile	
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275 280 285	
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Val Leu Asp Asp Val Trp Ser Glu Asn Arg Asp Asp Trp Glu Arg Leu	
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Thr Arg Asp Thr Lys Ile Ala Ser Ile Ile Gly Thr Met Lys Glu Ile				
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Cys Ala Phe Gly Ser Val Asn Pro Gln Glu His Leu Glu Leu Glu Val				
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Ile Gly Arg Lys Ile Ala Gly Lys Leu Lys Gly Ser Pro Leu Ala Ala				
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Arg Thr Ile Met Glu Ser Glu Val Trp Gln Leu Pro Gln Ala Glu Asn				
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Leu Arg Gln Cys Phe Ala Phe Cys Ala Val Phe His Lys Asp Tyr Leu				
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Phe Tyr Lys His Glu Leu Ile Gln Thr Trp Ile Ala Glu Gly Phe Ile				
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gca cat caa gga aac aag agg atg gaa gat gtc gga agc agc tac ttc				1440
Ala His Gln Gly Asn Lys Arg Met Glu Asp Val Gly Ser Ser Tyr Phe				
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cga tat gtg atg cat gac ctc ata cac gat ctt gcc caa ttt ata tca				1536
Arg Tyr Val Met His Asp Leu Ile His Asp Leu Ala Gln Phe Ile Ser				
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Val Gly Glu Cys His Arg Ile Asp Asp Asp Lys Ser Lys Glu Thr Pro				
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agt acg act cgt cat cta tca gta gca tta act gag caa atg aag ttg				1632
Ser Thr Thr Arg His Leu Ser Val Ala Leu Thr Glu Gln Met Lys Leu				
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Gln	Arg	Asn	Gln	Tyr	Pro	Tyr	Met	Thr	Lys	Val	Asn	Ser	Cys	Leu	Leu	
565			570			575										
cct	cat	agc	ttg	ttc	aaa	aga	ctg	aaa	aga	atc	cat	gtt	tta	gtt	ttg	1776
Pro	His	Ser	Leu	Phe	Lys	Arg	Leu	Lys	Arg	Ile	His	Val	Leu	Val	Leu	
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Gln	Lys	Cys	Gly	Met	Lys	Glu	Leu	Pro	Asp	Ile	Ile	Gly	Asp	Leu	Ile	
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Gln	Leu	Arg	Tyr	Leu	Asp	Ile	Ser	Tyr	Asn	Ala	Cys	Ile	Gln	Arg	Leu	
610			615			620										
ccc	gag	tca	ttg	tgc	gac	ctt	tac	aat	ctg	caa	gca	ctg	agg	cta	tgg	1920
Pro	Glu	Ser	Leu	Cys	Asp	Leu	Tyr	Asn	Leu	Gln	Ala	Leu	Arg	Leu	Trp	
625			630			635			640							
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Gly	Cys	Gln	Leu	Arg	Ser	Phe	Pro	Gln	Gly	Met	Ser	Lys	Leu	Ile	Asn	
645			650			655										
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660			665			670										
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675			680			685										
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725			730			735										
gag	tta	gag	tgg	gca	gct	ggc	cag	gtt	tcc	agc	ttg	gag	cat	gag	tta	2256
Glu	Leu	Glu	Trp	Ala	Ala	Gly	Gln	Val	Ser	Ser	Leu	Glu	His	Glu	Leu	
740			745			750										
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Cys Thr Arg Leu Glu Gly Leu Ser Tyr Ile Gly Gln Leu Pro His Leu	
805 810 815	
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820 825 830	
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835 840 845	
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Leu Val Leu Glu Asp Met Pro Thr Leu Lys Glu Phe Pro Asn Leu Ala	
850 855 860	
caa ctt cct tgt ctc aag att att cac atg aag aac atg ttt gca gta	2640
Gln Leu Pro Cys Leu Lys Ile Ile His Met Lys Asn Met Phe Ala Val	
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Lys His Ile Gly Arg Glu Leu Tyr Gly Asp Ile Glu Ser Asn Cys Phe	
885 890 895	
cta tca tta gaa gag ctt gtg ctg cag gac atg ctg aca ttg gag gaa	2736
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ctc cca aat ctt gga caa ctt cca cat ctt aag gtt att cac atg aag	2784
Leu Pro Asn Leu Gly Gln Leu Pro His Leu Lys Val Ile His Met Lys	
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930 935 940	
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1010		1015					1020									
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Ser	Trp	Ala	Glu	Arg	Glu	Glu	Leu	Phe	Ser	Cys	Leu	Cys	Arg	Leu		
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1100		1105					1110									
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Thr	Ala	Ser	Leu	Ser	Leu	Leu	His	Ile	Ile	Lys	Cys	Pro	Asn	Leu		
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aga	aat	ctg	gga	gaa	ggg	ttg	cta	tca	aac	cac	ctg	cca	cat	atc		3474
Arg	Asn	Leu	Gly	Glu	Gly	Leu	Leu	Ser	Asn	His	Leu	Pro	His	Ile		
1145		1150					1155									
aat	gct	att	cgg	ata	tgg	gaa	tgt	gct	gaa	ctg	ttg	tgg	ctg	cct		3519
Asn	Ala	Ile	Arg	Ile	Trp	Glu	Cys	Ala	Glu	Leu	Leu	Trp	Leu	Pro		
1160		1165					1170									
gtc	aag	agg	ttt	aga	gaa	ttc	acc	acc	ctt	gag	aac	ttg	tca	ata		3564
Val	Lys	Arg	Phe	Arg	Glu	Phe	Thr	Thr	Leu	Glu	Asn	Leu	Ser	Ile		
1175		1180					1185									
agg	aac	tgc	ccc	aag	ctc	atg	agc	atg	aca	cag	tgt	gag	gag	aat		3609
Arg	Asn	Cys	Pro	Lys	Leu	Met	Ser	Met	Thr	Gln	Cys	Glu	Glu	Asn		
1190		1195					1200									
gac	ctc	ctc	ctc	ccg	ccg	tta	atc	aag	gca	cta	gaa	ttg	ggt	gac		3654
Asp	Leu	Leu	Leu	Pro	Pro	Leu	Ile	Lys	Ala	Leu	Glu	Leu	Gly	Asp		

1205

1210

1215

tgt gga aat ctt ggg aaa tcg ctg cct gga tgc cta